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SEQUENCE LISTING

<110> Crucell Holland B.V.

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Bakker, Adrianus Q.

<120> AGONISTIC BINDING MOLECULES TO THE HUMAN OX40 RECEPTOR

<130> 0077 WO 00 ORD

<150> PCT/NL02/00389

<151> 2002-06-13

<160> 54

<170> PatentIn version 3.1

<210> 1

<211> 769

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02008

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<221> CDS

<222> (3)..(767)

<223>

<400> 1

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| Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln | |
| 1 5 10 15 | |

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| cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt | 95 |
| Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe | |
| 20 25 30 | |

agc aac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 143
 Ser Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 191
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
 50 55 60
 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 239
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75
 acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg 287
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 80 85 90 95
 tat tac tgt gcc aaa gac cgc tac tcc cag gtg cac tac gcg ttg gat 335
 Tyr Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp
 100 105 110
 tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt 383
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly
 115 120 125
 tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag 431
 Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln
 130 135 140
 atg acg cag tct cca gac tca ctg ccc gtc acc cct gga gag ccg gcc 479
 Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
 145 150 155
 tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac 527
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
 160 165 170 175
 aac tat ttg gat tgg tac ctg cag aag gca ggg cag tct cca cag ctc 575
 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu
 180 185 190
 ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 623
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 195 200 205
 agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg 671
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 210 215 220
 gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac tac aac cac 719
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His
 225 230 235
 ccg acg acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc 767
 Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 240 245 250 255
 gc 769

<210> 2

<211> 255

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02008

<400> 2

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30

Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
 115 120 125

Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
 130 135 140

Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
 145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn
 165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu Leu
 180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser
 195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
 210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His Pro
 225 230 235 240

Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 245 250 255

<210> 3

<211> 775

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02009

<220>

<221> CDS

<222> (3)..(773)

<223>

<400> 3

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| Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln | |
| 1 5 10 15 | |
| cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc | 95 |
| Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe | |
| 20 25 30 | |
| agc ggc tac tct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg | 143 |
| Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu | |
| 35 40 45 | |
| gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa | 191 |
| Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu | |
| 50 55 60 | |
| tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca | 239 |
| Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser | |
| 65 70 75 | |
| aag aac tca ctg tat ctg caa atg aac agt ctg aga gcc gag gac aca | 287 |
| Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr | |
| 80 85 90 95 | |
| gcc gtg tat tac tgt gcc aaa gac cgc tac gtc aac acg tcg aac gcg | 335 |
| Ala Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala | |
| 100 105 110 | |
| ttc gat tac tgg ggc cag gcc acc ctg gtg acc gtg ctc gag ggt acc | 383 |
| Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr | |
| 115 120 125 | |
| gga ggt tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac | 431 |
| Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp | |
| 130 135 140 | |
| atc cag atg aca cag tct cca gac tca ctg ccc gtc acc cct gga gag | 479 |
| Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu | |
| 145 150 155 | |

ccg gcc tcc atc tcc tgc aga tct agt cag agc ctc ctg cat agt aat 527
 Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn
 160 165 170 175
 gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca 575
 Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
 180 185 190
 cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac 623
 Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp
 195 200 205
 agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc 671
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
 210 215 220
 aga gtg gag gct cac cat gtt ggg gtt tat tac tgc cag cag tac ccg 719
 Arg Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro
 225 230 235
 ctg ggc ccg ccc acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc 767
 Leu Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 240 245 250 255
 gcg gcc gc 775
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<210> 4

<211> 257

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02009

<400> 4

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30
 Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
 50 55 60
 Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
 65 70 75 80
 Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe
 100 105 110
 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
 115 120 125
 Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile
 130 135 140
 Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro
 145 150 155 160
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
 165 170 175
 Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
 180 185 190
 Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg
 195 200 205
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
 210 215 220
 Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro Leu
 225 230 235 240
 Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala
 245 250 255

Ala

<210> 5

<211> 736

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02010

<220>

<221> CDS

<222> (3) .. (734)

<223>

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1 5 10 15
cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30
agc ggc tac cct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 143
Ser Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45
gag tgg gtg gca gtt ata tca tat gat gga agt aat aaa tac tac gca 191
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
50 55 60
gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac 239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75
acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg 287
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
80 85 90 95
tat tac tgt gca aga gac atg tcc ggc ttc cac gag ttc gat tac tgg 335
Tyr Tyr Cys Ala Arg Asp Met Ser Gly Phe His Glu Phe Asp Tyr Trp
100 105 110
ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc 383
Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly
115 120 125
gga acc ggg tct ggg act ggt acg agc gag ctc acc cag tct cca tcc 431
Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser
130 135 140
tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca 479
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145 150 155
agt cag agc att agc agc tac tta aat tgg tat cag cag aaa cca ggg 527
Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
160 165 170 175
aaa gcc cct aag ctc ctg atc tat gct gca tcc agt ttg caa agt ggg 575
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
180 185 190
gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc 623
Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205
acc atc agc agt ctg caa cct gaa gat ttt gca act tac tac tgt caa 671
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220
cag agt tac agt acc cct cca acg ttc ggc caa ggg acc aag gtg gag 719
Gln Ser Tyr Ser Thr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
225 230 235
atc aaa cgt gcg gcc gc 736
Ile Lys Arg Ala Ala
240

<210> 6

<211> 244

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02010

<400> 6

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro
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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asp Met Ser Gly Phe His Glu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys Arg Ala Ala

<210> 7

<211> 763

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02011

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<221> CDS

<222> (3)..(761)

<223>

<400> 7

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| Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln | |
| 1 5 10 15 | |
| cct ggg agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc | 95 |
| Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe | |
| 20 25 30 | |
| agc gac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg | 143 |
| Ser Asp Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu | |
| 35 40 45 | |
| gag tgg gtc tca tcc att agt ggt ggt agc aca tac tac gca gac tcc | 191 |
| Glu Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser | |
| 50 55 60 | |
| agg aag ggc aga ttc acc atc tcc aga gac aat tcc aag aac acg ctg | 239 |
| Arg Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu | |
| 65 70 75 | |
| tat ctt caa atg aac aac ctg aga gct gag gac acg gcc gtg tat tac | 287 |
| Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr | |
| 80 85 90 95 | |
| tgt gca aga gac cgc tac ttc agg cag cag aac gcg ttc gat tac tgg | 335 |
| Cys Ala Arg Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp | |
| 100 105 110 | |
| ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc ggc | 383 |
| Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly | |
| 115 120 125 | |

gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag atg act 431
 Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr
 130 135 140

cag tct cca gtc acc ctg ccc gtc acc cct gga gag ccg gcc tcc atc 479
 Gln Ser Pro Val Thr Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile
 145 150 155

tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac aac tat 527
 Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
 160 165 170 175

ttg gat tgg tac ctg cag aag cca ggg cag tct cca cag ctc ctg atc 575
 Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
 180 185 190

tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc agt ggc 623
 Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205

agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg gag gct 671
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 210 215 220

gag gat gtt ggg gtt tat tac tgc cag cag tac ctc acg gcc ccg ccc 719
 Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Leu Thr Ala Pro Pro
 225 230 235

acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc gc 763
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
 240 245 250

<210> 8

<211> 253

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02011

<400> 8

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
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Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Asp Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Trp Val Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Val Thr Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu
165 170 175

Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
180 185 190

Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
210 215 220

Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Leu Thr Ala Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala
245 250

<210> 9

<211> 748

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02012

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<221> CDS

<222> (3)..(746)

<223>

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Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
1 5 10 15
ccg ggt ggc agc ctg cgc ctg agc tgc gcc gct agc ggc ttc acc ttt 95
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
20 25 30
agc aac gac tcg atg aac tgg atg cgc cag gcc ccg ggc aaa ggc ctc 143
Ser Asn Asp Ser Met Asn Trp Met Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45
gaa tgg gtg gcc aat atc aat cag gat ggc aac gaa aaa tat tac gcc 191
Glu Trp Val Ala Asn Ile Asn Gln Asp Gly Asn Glu Lys Tyr Tyr Ala
50 55 60
gac tct gtc aaa ggc cgc ttc acc atc agt cgc gat aac tcc aaa aac 239
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75
tcc ctg tac ctg cag atg aac agc ctg cgc gac gaa gat acc gcc ctg 287
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Leu
80 85 90 95
tac tac tgc gca cgc gcc cgc gcc gcc ggc acc atc ttc gat tac tgg 335
Tyr Tyr Cys Ala Arg Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr Trp
100 105 110
ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt tcc gcc 383
Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly
115 120 125
gga acc ggg tct ggg act ggt acg agc gag ctc gat atc cag atg acc 431
Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr
130 135 140
cag agc ccg agt tcc ctg agc gcc tcc gtg ggc gac cgc gtg acc atc 479
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155
acc tgc cgc gcc agc cag aac gtc agc aac tac ctg acc tgg tac cag 527
Thr Cys Arg Ala Ser Gln Asn Val Ser Asn Tyr Leu Thr Trp Tyr Gln
160 165 170 175
cag aaa ccg ggc aag gct ggc aaa ctg ctg att tac gcc gcc agc agc 575
Gln Lys Pro Gly Lys Ala Gly Lys Leu Ile Tyr Ala Ala Ser Ser
180 185 190
ctc caa agc ggc gtg ccg tct aga ttc agt ggc tcc gcc tcc gga acc 623
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Gly Thr
195 200 205
gat ttt acc ctg acc atc agc agc ctg cag ccg gaa gat ttc gct acc 671
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220
tac tat tgt cag cag tcc tac ttc aac ccg gcg acc ttc ggc cag ggc 719
Tyr Tyr Cys Gln Gln Ser Tyr Phe Asn Pro Ala Thr Phe Gly Gln Gly
225 230 235
acc aaa ctg gaa atc aaa cgc gcg gcc gc 748
Thr Lys Leu Glu Ile Lys Arg Ala Ala
240 245

<210> 10

<211> 248

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02012

<400> 10

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Asn Asp Ser Met Asn Trp Met Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Trp Val Ala Asn Ile Asn Gln Asp Gly Asn Glu Lys Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Leu Tyr
85 90 95

Tyr Cys Ala Arg Ala Arg Ala Ala Gly Thr Ile Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser Gly Gly
115 120 125

Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

Cys Arg Ala Ser Gln Asn Val Ser Asn Tyr Leu Thr Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Lys Ala Gly Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
180 185 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 210 215 220

Tyr Cys Gln Gln Ser Tyr Phe Asn Pro Ala Thr Phe Gly Gln Gly Thr
 225 230 235 240

Lys Leu Glu Ile Lys Arg Ala Ala
 245

<210> 11

<211> 769

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02021

<220>

<221> CDS

<222> (3)..(767)

<223>

<400> 11

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| Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln | |
| 1 5 10 15 | |
| cct agg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt | 95 |
| Pro Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe | |
| 20 25 30 | |
| agc agc tac gcg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg | 143 |
| Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu | |
| 35 40 45 | |
| gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac gca | 191 |
| Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala | |
| 50 55 60 | |
| gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac | 239 |
| Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn | |
| 65 70 75 | |
| acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg | 287 |
| Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val | |
| 80 85 90 95 | |
| tat tac tgt gcc aaa gac cgc tac atc acg ttg ccg aac gcg ttg gat | 335 |
| Tyr Tyr Cys Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp | |
| 100 105 110 | |
| tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc gga ggt | 383 |
| Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly | |
| 115 120 125 | |

tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag 431
 Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln
 130 135 140

atg acc cag tct cca gtc tca ctg ccc gtc acc cct gga gag ccg gcc 479
 Met Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
 145 150 155

tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac 527
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
 160 165 170 175

aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca cag ctc 575
 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
 180 185 190

ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 623
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 195 200 205

agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg 671
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 210 215 220

gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac aag tcg aac 719
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Lys Ser Asn
 225 230 235

ccg ccc acc ttc ggc cag ggc acc aaa gtg gaa atc aaa cgc gcg gcc 767
 Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
 240 245 250 255

gc 769

<210> 12

<211> 255

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02021

<400> 12

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 1 5 10 15

Arg Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 20 25 30

Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly Gly Ser
115 120 125

Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn
165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu
180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser
195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Lys Ser Asn Pro
225 230 235 240

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
245 250 255

<210> 13

<211> 745

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02022

<220>

<221> CDS

<222> (3) .. (743)

<223>

<400> 13

| | |
|---|-----|
| cc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cat | 47 |
| Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His | |
| 1 5 10 15 | |
| cct ggg ggg tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc | 95 |
| Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe | |
| 20 25 30 | |
| agt agc tat gct atg cac tgg gtt cgc cag gct cca gga aaa ggt ctg | 143 |
| Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu | |
| 35 40 45 | |
| gag tgg gta tca gct att ggt acc ggt ggt ggc aca tac tat gca gac | 191 |
| Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Thr Tyr Tyr Ala Asp | |
| 50 55 60 | |
| tcc gtg cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc | 239 |
| Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser | |
| 65 70 75 | |
| ttg tat ctt caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat | 287 |
| Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr | |
| 80 85 90 95 | |
| tac tgt gca aga tac gac gag ccg ctg acg att tac tgg ttt gac tcc | 335 |
| Tyr Cys Ala Arg Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser | |
| 100 105 110 | |
| tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca | 383 |
| Trp Gly Gln Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser | |
| 115 120 125 | |
| ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag | 431 |
| Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln | |
| 130 135 140 | |
| tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc | 479 |
| Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser | |
| 145 150 155 | |
| tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg tac caa cag | 527 |
| Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln | |
| 160 165 170 175 | |
| aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg | 575 |
| Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg | |
| 180 185 190 | |
| gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac | 623 |
| Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp | |
| 195 200 205 | |
| ttc act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat | 671 |
| Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr | |
| 210 215 220 | |
| tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc | 719 |
| Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr | |
| 225 230 235 | |
| aag gtg gag atc aaa cgt gcg gcc gc | 745 |
| Lys Val Glu Ile Lys Arg Ala Ala | |
| 240 245 | |

<210> 14

<211> 247

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02022

<400> 14

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser
50 55 60

Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Tyr Asp Glu Pro Leu Thr Ile Tyr Trp Phe Asp Ser Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala
180 185 190

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
 210 215 220

Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys
 225 230 235 240

Val Glu Ile Lys Arg Ala Ala
 245

<210> 15

<211> 745

<212> DNA

<213> Artificial sequence

<220>

<223> scFv SC02023

<220>

<221> CDS

<222> (3)..(743)

<223>

<400> 15

cc atg gcc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cat 47
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His
 1 5 10 15

cct ggg ggg tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc 95
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
 20 25 30

agt agc tat gct atg cac tgg gtt cgc cag gct cca gga aaa ggt ctg 143
 Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45

gag tgg gta tca gct att ggt act ggt ggt ggc aca tac tat gca gac 191
 Glu Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp
 50 55 60

tcc gtg atg ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg 239
 Ser Val Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 65 70 75

ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat 287
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 80 85 90 95

tac tgt gca aga tac gac aat gtg atg ggt ctt tac tgg ttt gac tac 335
 Tyr Cys Ala Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr
 100 105 110

tgg ggc caa ggt acc ctg gtc acc gtc tcg agt ggt gga ggc ggt tca 383

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125
 ggc gga ggt ggc tct ggc ggt ggc gga tcg gaa att gag ctc aca cag 431
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln
 130 135 140
 tct cca gcc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc tcc 479
 Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
 145 150 155
 tgc agg gcc agt cag agt gtt agc agc tac tta gcc tgg tac caa cag 527
 Cys Arg Ala Ser Gln Ala Pro Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
 160 165 170 175
 aaa cct ggc cag gct ccc agg ctc ctc atc tat gat gca tcc aac agg 575
 Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg
 180 185 190
 gcc act ggc atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gac 623
 Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205
 ttc act ctc acc atc agc agc cta gag cct gaa gat ttt gca gtt tat 671
 Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr
 210 215 220
 tac tgt cag cag cgt agc aac tgg cct ccg gct ttc ggc gga ggg acc 719
 Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr
 225 230 235
 aag gtg gag atc aaa cgt gcg gcc gc 745
 Lys Val Glu Ile Lys Arg Ala Ala
 240 245

<210> 16

<211> 247

<212> PRT

<213> Artificial sequence

<220>

<223> scFv SC02023

<400> 16

Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro
 1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser
 20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Val Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser
 50 55 60

Val Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Glu Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala
180 185 190

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
210 215 220

Cys Gln Gln Arg Ser Asn Trp Pro Pro Ala Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys Arg Ala Ala
245

<210> 17

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02008

<400> 17

Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr
1 5 10

<210> 18

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02009

<400> 18

Asp Arg Tyr Val Asn Thr Ser Asn Ala Phe Asp Tyr
1 5 10

<210> 19

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02010

<400> 19

Asp Met Ser Gly Phe His Glu Phe Asp Tyr
1 5 10

<210> 20

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02011

<400> 20

Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr
1 5 10

<210> 21

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02012

<400> 21

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Ala | Ala | Gly | Thr | Ile | Phe | Asp | Tyr |
| 1 | | | | 5 | | | | | 10 |

<210> 22

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02021

<400> 22

| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Tyr | Ile | Thr | Leu | Pro | Asn | Ala | Leu | Asp | Tyr |
| 1 | | | | 5 | | | | | | 10 | |

<210> 23

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02022

<400> 23

| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asp | Glu | Pro | Leu | Thr | Ile | Tyr | Trp | Phe | Asp | Ser |
| 1 | | | | 5 | | | | | | 10 | |

<210> 24

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> CDR3 of scFv SC02023

<400> 24

Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr
 1 5 10

<210> 25

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 008

<400> 25

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 26

<211> 449

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 011

<400> 26

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Asp Arg Tyr Phe Arg Gln Gln Asn Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 27

<211> 451

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain 021

<400> 27

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Arg Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Arg Tyr Ile Thr Leu Pro Asn Ala Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 28

<211> 450

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of heavy chain of 023

<400> 28

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Met
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Tyr Asp Asn Val Met Gly Leu Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 29

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 008

<400> 29

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
85 90 95

Tyr Asn His Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 30

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 011

<400> 30

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
85 90 95

Tyr Asn His Pro Thr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 31

<211> 219

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 021

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
85 90 95

Lys Ser Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 32

<211> 214

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence of light chain of 023

<400> 32

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 33

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZalphaB

<220>

<221> CDS

<222> (1)..(54)

<223>

<400> 33

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tct | ctc | gag | aaa | aga | gag | gct | gaa | gct | gca | gga | att | cac | gtg | gcc | cag | 48 |
| Ser | Leu | Glu | Lys | Arg | Glu | Ala | Glu | Ala | Ala | Gly | Ile | His | Val | Ala | Gln | |
| 1 | | | 5 | | | | 10 | | | | 15 | | | | | |

ccg gcc g

55

Pro Ala

<210> 34

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZalphaB

<400> 34

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Glu | Lys | Arg | Glu | Ala | Glu | Ala | Ala | Gly | Ile | His | Val | Ala | Gln |
| 1 | | | 5 | | | | 10 | | | | 15 | | | | |

Pro Ala

<210> 35

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFVH

<220>

<221> CDS

<222> (1)..(54)

<223>

<400> 35

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tct | ctc | gag | aaa | aga | gcc | atg | gaa | gct | gca | gga | att | cac | gtg | gcc | cag | 48 |
| Ser | Leu | Glu | Lys | Arg | Ala | Met | Glu | Ala | Ala | Gly | Ile | His | Val | Ala | Gln | |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | | |

| | | | |
|-----|-----|---|----|
| ccg | gcc | g | 55 |
| Pro | Ala | | |

<210> 36

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> 5' cloning site of pPicZFVH

<400> 36

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Glu | Lys | Arg | Ala | Met | Glu | Ala | Ala | Gly | Ile | His | Val | Ala | Gln |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |

Pro Ala

<210> 37

<211> 92

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic hinge region

<220>

<221> CDS

<222> (1) .. (90)

<223>

<400> 37

```

gcg gcc gcg cca aag cca agt acc cca cca ggt tct tca tgt cca cca      48
Ala Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro
1           5           10           15

```

```

tgt cca ggc tct ggc ggt gcg cca atc gat agc ggc ttt cta ga      92
Cys Pro Gly Ser Gly Gly Ala Pro Ile Asp Ser Gly Phe Leu
          20           25           30

```

<210> 38

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic hinge region

<400> 38

```

Ala Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro Pro
1           5           10           15

```

```

Cys Pro Gly Ser Gly Gly Ala Pro Ile Asp Ser Gly Phe Leu
          20           25           30

```

<210> 39

<211> 1416

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 008

<400> 39

```

atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga attctccatg      60
gccgaggtgc agctggtgga gtctggggga ggcttggtcc agcctggagg gtccctgaga      120
ctctcctgtg cagcctcttg attcaccttt agcaactaca cgatgaactg ggtccgccag      180
gcgcccggga aggggctgga gtgggtctca gctattagtg gtagtggtgg tagcacatac      240
tacgcagact ccgtgaaggg ccggttcacc atctccagag acaattccaa gaacacgctg      300
tatctgcaaa tgaacagcct gagagccgag gacacggccg tgtattactg tgccaaagac      360

```

```

cgctactccc aggtgcacta cgcgttgat tactggggcc agggcaccct ggtgaccgtc 420
tcctcagcct ccaccaagg ccctcggtc tccccctgg caccctctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttccccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagagagtt 720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780
gggggaccgt cagtcttctt cttccccca aaacccaagg acaccctcat gatctcccg 840
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 960
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggtgaat 1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg 1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
cccgctgtgg actccgacgg ctcttcttc ctctatagca agctcaccgt ggacaagagc 1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
tacacgcaga agagcctctc cctgtctccg ggtaaa 1416

```

<210> 40

<211> 1410

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 011

<400> 40

```

atggcatgcc ctggcttctt gtgggcactt gtgatctcca cctgtcttga attctccatg 60
gccgagggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga 120
ctctcctgtg cagcctctgg attcaccttc agcgactaca cgatgaactg ggtccgccag 180
gcgccccggga aggggctgga gtgggtctca tccattagtgt gtggtagcac atactacgca 240
gactccagga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 300
caaatgaaca acctgagagc tgaggacacg gccgtgtatt actgtgcaag agaccgctac 360
ttcaggcagc agaacgcgtt cgattactgg ggccagggca ccctggtgac cgtctctca 420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

```

```

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg    540
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggtgtcct acagtctca    600
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc    660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc    720
aaatcttgtg acaaaactca cacatgccc cctgtcccag cacctgaact cctgggggga    780
ccgtcagtct tcctcttccc ccaaaaccc aaggacaccc tcatgatctc ccggaccct    840
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg    900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggaggg gcagtacaac    960
agcacgtacc gtgtggtcag cgtcctcacc gtccctgcacc aggactggct gaatggcaag   1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag   1140
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc   1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg   1260
ctggactccg acggctcctt ctctctctat agcaagctca ccgtggacaa gagcaggtgg   1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   1380
cagaagagcc tctccctgtc tccgggtaaa                                1410

```

<210> 41

<211> 1416

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 021

<400> 41

```

atggcatgcc ctggcttctt gtgggcactt gtgatctcca cctgtcttga attctccatg    60
gccgaggtgc agctgggtga gtctggggga ggcttggtac agcctagggg gtccctgaga   120
ctctcctgtg cagcctctgg attcaccttt agcagctacg cgatgaactg ggtccgccag   180
gcgcccggga aggggctgga gtgggtggca gttatatcat atgatggaag caataaatac   240
tacgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg   300
tatctgcaaa tgaacagcct gagagctgag gacacagccg tgtattactg tgccaaagac   360
cgctacatca cgttgccgaa cgcgttggtg tactggggcc agggcaccct ggtgaccgtc   420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc   480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg   540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttccgggc tgtcctacag   600

```



```

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaaag cccagcaaca ccaaggtgga caagagagtt 720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 780
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 840
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagcccg ggaggagcag 960
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080
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gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
cccgtgctgg actccgacgg ctccctcttc ctctatagca agctcaccgt ggacaagagc 1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
tacacgcaga agagcctctc cctgtctccg ggtaaa 1416

```

<210> 42

<211> 1413

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of heavy chain of 023

<400> 42

```

atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga attctccatg 60
gccgagggtgc agctgggtgga gtctggggga ggcttggtac atcctggggg gtccctgaga 120
ctctcctgtg caggctctgg attcaccttc agtagctatg ctatgcactg ggttcgccag 180
gctccaggaa aaggctctgga gtgggtatca gctattggta ctggtggtgg cacatactat 240
gcagactccg tgatgggccg gttcaccatc tccagagaca attccaagaa cagctgtat 300
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc aagatacgac 360
aatgtgatgg gtctttactg gtttgactac tggggccagg gcaccctggt gaccgtctcc 420
tcagcctcca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct 480
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 540
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggtgt cctacagtcc 600
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccacg 660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttag 720

```

```

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840
cctgaggtca catgctgtgt ggtggacgtg agccacgaag accctgaggt caagttcaac 900
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960
aacagcacgt accgtgttgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag 1140
gagatgacca agaaccaggt cagcctgacc tgctgtgtca aaggcttcta tcccagcgac 1200
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1260
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1320
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380
acgcagaaga gcctctccct gtctccgggt aaa 1413

```

<210> 43

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 008

<400> 43

```

atggcatgcc ctggcttctt gtgggcactt gtgatctcca cctgtctcga gttttccatg 60
gctgacatcg tgatgacaca gtctccagac tcaactgccg tcaccctgg agagccggcc 120
tccatctctt gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttgat 180
tggtacctgc agaaggcagg gcagtctcca cagctcctga tctatttggg ttctaatacgg 240
gcctccgggg tcctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 300
atcagcagag tggaggctga ggatgttggg gtttattact gccagcagta ctacaaccac 360
ccgacgacct tcggccaggg caccaaactg gaaatcaaac gtactgtggc tgcaccatct 420
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtga taacgccctc 540
caatcggtga actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc 600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660
gaagtcaccc atcagggcct gagctcgccc gtcacaaaaga gcttcaacag gggagagtgt 720

```

<210> 44

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 011

<400> 44

```
atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtctcga gttttccatg    60
gctgacatcg tgatgacaca gtctccagtc accctgcccg tcaccctgg agagccggcc    120
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat    180
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaacggy    240
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa    300
atcagcagag tggaggctga ggatgttggg gtttattact gccagcagta cctcacggcc    360
ccgccacct tcggccaggg caccaaactg gaaatcaaac gtactgtggc tgcaccatct    420
gtcttcacat tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc    480
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtga taacgccctc    540
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc    600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc    660
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt    720
```

<210> 45

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of light chain of 021

<400> 45

```
atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtctcga gttttccatg    60
gctgacatcc agatgaccca gtctccagtc tcaactgccg tcaccctgg agagccggcc    120
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat    180
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaacggy    240
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa    300
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